



SEQUENCE LISTING

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<110> Hauptmann, Rudolph
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Maurer-Pary, Ingrid
Stratowa, Christian

<120> TNF Receptors, TNF Binding Proteins and DNAs Coding for
Them

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<140> 0,3525,919

<141> 2000-03-15

<150> 09,383,616

<151> 1991-02-01

<152> 0,151,217

<153> 1991-11-17

<154> 0,821,710

<155> 1992-01-02

<156> 67,511,410

<157> 1996-04-10

<160> 87

<170> PatentIn Ver. 2.0

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<221> CDS

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<232> (1)..(87)

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<241> misc_feature

<242> (88)..(1,0)

<243> Portion of TNF-BF pro protein cleaved by
extracellular proteases following secretion.

<250>

<251> misc_feature

<252> (606)..(633)

<253> Portion of TNF-BF pro protein cleaved by
extracellular proteases following secretion.

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gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct	96
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro	
20 25 30	
ccc ata ggg gac agt gag aac cca gat agt ggg tgt ccc caa aga aat	144
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys	
35 40 45	
tat atc cag cct caa aat aat tgg att tgc tgt acc aag tgc cag aat	192
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys	
50 55 60	
gga acc tac ttg tac aat gac tgt cca gga cag gag cag gat acg gac	240
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp	
65 70 75 80	
tgc agg gag tgt gag agc ggc ttc ttc acc gct tca gaa aac cag ctc	288
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu	
85 90 95	
aga cac tgc ctc agc tgc tcc aat tgc cga aag gaa atg ggt cag gtg	336
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val	
100 105 110	
gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg	384
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg	
115 120 125	
aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc	432
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe	
130 135 140	
aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc acc tgc cag gag	480
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu	
145 150 155 160	
aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttc ata aga gaa	528
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu	
165 170 175	
aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc aag	576
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr	
180 185 190	
aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca	624
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser	
195 200 205	
ggc aac aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt	672
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu	
210 215 220	
tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag	720

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys	
225 230 235 240	
taa agc ctc tac tcc att gtt tgt ggg aaa tgg gaa cct gaa aaa gag	768
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Gln Lys Gln	
245 250 255	
ggg gag ctt gaa gga act act act aag tcc ctg ggc cca aac cca agc	816
Gly Glu Leu Gln Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser	
260 265 270	
ctc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtc	864
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val	
275 280 285	
ccc agt tcc acc ttc acc tcc agc ttc acc tat acc ccc agt gac tgc	912
Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys	
290 295 300	
ccc aac ttt gag gct ccc cgc aga gag gtg gca cca ccc tat cag ggg	960
Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly	
305 310 315 320	
gct gac ccc atc ctt gag aca gct ctg gcc tcc gac ccc atc ccc aac	1008
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn	
325 330 335	
ccc ctt cag aag tgg gag gac agc gcc ccc aag cca cag agc cta gac	1056
Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp	
340 345 350	
act gat gac ccc gag aag ctg tac gcc gtg gtg gag aac gtg ccc ccg	1104
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Gln Asn Val Pro Pro	
355 360 365	
tgg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac ccc gag	1152
Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu	
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Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Gln Ala Gln	
385 390 395 400	
tac agc atg ctg gag acc tgg aag cgg cgc acc cgg cgg tgc gag gcc	1248
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala	
405 410 415	
aag ctg gag ctg ctg gga cgc gtg ctg cgc gac atg gac ctg ctg ggc	1296
Thr Leu Gln Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly	
420 425 430	
tgt ctg gag gac atc gag gag gcc att tgc gcc ccc gcc gcc ctg ccg	1344
Cys Leu Gln Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro	
435 440 445	
ccc gcc ccc agt ctt ctg aga tga	1368
Pro Ala Pro Ser Leu Leu Arg	

450

455

210 - 2
 211 - 495
 212 - 1KT
 213 - Homo sapiens

400 - 2

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Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
 20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
 65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
 180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
 195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
 210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
 225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
 245 250 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
 260 265 270
 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
 275 280 285
 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
 290 295 300
 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
 305 310 315 320
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
 325 330 335
 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
 340 345 350
 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
 355 360 365
 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
 370 375 380
 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
 385 390 395 400
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
 405 410 415
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
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 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
 435 440 445
 Pro Ala Pro Ser Leu Leu Arg
 450 455

42100-3
 42110-483
 42120-DNA
 42130-Homo sapiens

42100-
 42110-CDS
 42120-(1)..(483)

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 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt 96
 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
 20 25 30

cca agc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 144
 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
 35 40 45

ttc acc ggt tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa 192
 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
 50 55 60

tgc cga aag gaa atg ggt cag gtc gag atc tat tat tgc aca gtc gac 240
 Cys Arg Lys Glu Met Gly Gln Val Gln Ile Ser Ser Cys Thr Val Asp
 65 70 75 80

cag aac acc gtc tat ggc tgc aag aag aar cag tac cga cat tat tgc 288
 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
 85 90 95

agt aaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat gag 336
 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
 100 105 110

acc atc aac ctc tcc tgc cag gag aaa cag aac acc gtc tgc acc tgc 384
 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
 115 120 125

cat cca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac 432
 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
 130 135 140

tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag 480
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 35 40 45

Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
 50 55 60

Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
 65 70 75 80

Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
 85 90 95
 Ser Gln Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
 100 105 110
 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
 115 120 125
 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
 130 135 140
 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
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 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga 87
 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly
 20 25

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 <113> Homo sapiens

<100> 6
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 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly
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 <112> DNA
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1 5 10

33

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<221> 11
<222> PRT
<223> Homo sapiens

<220> 8
Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg
1 5 10

<221> 9
<221> 20
<222> DNA
<223> Homo sapiens

<220>
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<222> (1)..(30)

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Val Lys Gly Thr Glu Asp Ser Gly Thr Thr
1 5 10

30

<221> 10
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<222> PRT
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<220> 10
Val Lys Gly Thr Glu Asp Ser Gly Thr Thr
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<221> 11
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<223> Artificial Sequence

<220>
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 ctggacagac caggtccagg gaagcccag cactgacgtt cccacactgc cctgagccca 180
 aatggggagag tggagggcca taactgtctg gc atg ggc ctg tcc acc gtg cct 237
 Met Gly Leu Ser Thr Val Phe
 1 5
 gac ctg ctg atg cca atg gtg ctg ctg gag ctg ttg gtg gga ata tac 281
 Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr
 10 15 20
 ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329
 Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys
 25 30 35
 aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377
 Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
 40 45 50 55
 tgg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425
 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
 60 65 70
 tgt cca ggc cag ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473
 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
 75 80 85
 tcc ttc acc gct tca gaa aac cac ctg aga cac tgc ctg agc tgc tcc 521
 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
 90 95 100
 aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569
 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
 105 110 115
 gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat 617
 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
 120 125 130 135
 tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctg tgc ctg aat 665
 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn
 140 145 150
 ggg acc gta cac ctg tcc tgc cag gag aaa cag aac acc gtg tgc acc 713
 Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Phe
 155 160 165
 tgc cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt 761
 Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser
 170 175 180
 aac tgt aag aaa agc ctg gag tgc acc aag ttg tgc cta ccc cag att 809

Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile
 131 190 195

agg aat att aat acg act gag gac tca ggt acc acc gta atg ttg ccc 897
 Glu Asn Val Lys Gly Thr Gln Asp Ser Gly Thr Thr Val Leu Leu Pro
 196 205 210 215

atg gta att ttc att ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt 905
 Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly
 220 225 230

tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt 953
 Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val
 235 240 245

tgt ggg aaa tgg acc cct gag aaa gag ggg gag ctt gaa gaa act act 1001
 Cys Gly Lys Ser Thr Pro Gln Lys Gln Gly Gln Leu Glu Gly Thr Thr
 250 255 260

act aag cca atg acc cca aac cca agc ttc agt ccc act cca ggc ttc 1049
 Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe
 265 270 275

acc ccc acc cag ggc ttc agt ccc gtc ccc agt tcc acc ttc acc tcc 1097
 Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser
 280 285 290 295

agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc 1145
 Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg
 300 305 310

aga gag gtg gaa cca ccc tat cag ggg gct gac ccc atc ctt gcg aca 1193
 Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr
 315 320 325

gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac 1241
 Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp
 330 335 340

agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acg ctg 1289
 Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu
 345 350 355

tac gcc gtg gtg gag aac gtg ccc ccg ttg cgc tgg aaggaattc 1334
 Tyr Ala Val Val Gln Asn Val Pro Pro Leu Arg Trp
 360 365 370

<210> 12

<211> 371

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA insert of
 lambdaTNF-BP15 and pTNF-BP15 vectors

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Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
100 105 110

Glu Ile Ser Ser Cys Thr Val A.p Arg Asp Thr Val Cys Gly Cys Arg
115 120 125

Lys Asn Gln Tyr Arg His Tyr Tip Ser Glu Asn Leu Phe Gln Cys Phe
130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Pro Lys
225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
245 250 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Ile Ile Pro Asn
325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
355 360 365

Leu Arg Trp
370

4210- 13

4211- 6414

4212- DNA

4213- Artificial Sequence

4220-

4221- Description of Artificial Sequence: pADCMV1 vector

4222-

4223- unsure

4224- (344)

4225- "n" can be a, g, c, or t

4226-

4227- unsure

4228- (4157)

4229- "n" can be a, g, c, or t

4230-

4231- unsure

4232- (5135)

4233- "n" can be a, g, c, or t

4234-

4235- unsure

4236- (6255)

4237- "n" can be a, g, c, or t

4400- 13

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cccatatatg gagttccggg ttacataact tacggtaaatt ggcccgcctc gctgaccgcc 120

gaagagcccc cggccattga cgtcaataat gacgtatggt cccatagtaa cggcaatagg 180

gaatttccat tgaagtcgat ggggtggagta tttaaggtaa actgcccaact tggcagtgaca 240

tcaattgtat catatgccaa gtaagccccc tattgacgtc aatgacggta aatggccggc 300

ctgggattat gccacgtaca tgaccttatg ggactttcct actnggcagt acattctagt 360

attagtcate gctattacca tgggtatgag gttttggag tacctcaatg gggtgggata 420
 tgggtttgac tcaaggagat ttccaagtct caaccgcatt gacgtcaatg ggaattttgt 480
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 tgttttgcta ttttagatto caacctatgg aactgatgaa tgggagcagt ggtggaatgc 900
 atttaatgag gaaaactgt tttgtcaga agaaatgcca tctagtgtg atgaggtac 960
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 aaaatatttg atgtatagtg ccttgactag agatcataat cagccatacc acattttgag 1200
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 ggaacgcct ggtatcttta tagtctgtc ggggttcgcc acctctgact tgagcgtcga 6360
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<10> 14
 <11> 2173
 <12> DNA
 <13> Artificial Sequence

<10>
 <11> CDS
 <12> (245)..(1630)

<10>
 <13> Description of Artificial Sequence: raTNF-R8

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 gggtcaccg tgcacacacc cgggcaccc gtcccgatcg tcttaactca ttcaccagcg 180
 ttgcacattg ctgcctctgc ccagcccca atgggggagt gagagagcc aatgcgcgc 240
 ggac atg ggt ctc ccc atc gtg cct ggc ctg ctg ctg tca ctg gtg ctc 280
 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu
 1 5 10 15

atg gct ctg ctg atg ggg ata cac cca tca ggg gtc acc gga ctg gtt	337
Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val	
20 25 30	
cct tct att ggt gac agg gac aag agg gat aat ttg tgt ccc cag gga	385
Pro Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly	
35 40 45	
aag tat gcc cat cca aag aat aat tcc ata tcc tgg acc aag tgc cac	433
Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His	
50 55 60	
aaa gga acc tcc ttg ttg agt gac tgt cca acc cca gga cat gaa acc	481
Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr	
65 70 75	
gtc tgc gag ctg tct cat aac ggc acc ttt acc gct tcc cag aac cac	529
Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His	
80 85 90 95	
gtc aga cag tgt ctg aat tcc aag aca tgt cgg aaa gaa atg ttc cag	577
Val Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln	
100 105 110	
gtg gag att cct cct tcc aaa gct gac atg gac acc gtg tgt gcc tgc	625
Val Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys	
115 120 125	
aag aag aac caa ttc cag ccc tcc ctg agt gag acg cat ttc cag tgt	673
Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys	
130 135 140	
gtg gac tgc agc ccc tcc ttc aat ggc acc gtg aca atc ccc tgt aag	721
Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys	
145 150 155	
gag aaa cag aac acc gtg tgt aac tgc cac gca gga ttc ttt cta agc	769
Glu Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser	
160 165 170 175	
gga aat gag tgc acc cct tgc agc cac tgc aag aaa aat cag gaa tgt	817
Gly Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys	
180 185 190	
atg aag ctg tgc cta cct cca gtt gca aat gtc aca aac ccc cag gac	865
Met Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp	
195 200 205	
tca ggt act gcc gtg ctg ttg cct ctg gtt atc ttc cta ggt att tgc	913
Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys	
210 215 220	
att tta ttc ttt atc tgc atc aat cta ctg tgc cga tat ccc cag tgg	961
Leu Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp	
225 230 235	

agg ccc agg gtc tac tcc atc att tgt agg gat tca gct cct gtc aaa	1009
Arg Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys	
240 245 255	
acc gta aac att caa gga att att act aag cca ata act caa ggc tct	1057
Glu Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Ile Ala Ser	
260 265 270	
atc cca ggc ttc aac cca aac ccc ggc ttc aac ccc act cca ggc ttc	1105
Ile Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu Gly Phe	
275 280 285	
age aac aac cca ccc ttc agt cat cct gtc tcc act aac ccc atc age	1153
Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr Pro Ile Ser	
290 295 300	
ccc gtc ttc ggt cct agt aac tgg ccc aac ttc gtc cca cct gta aga	1201
Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg	
305 310 315	
gag gtg gtc cca aac cag ggt gct gac cct ctc ctc tac gga tcc ctc	1249
Glu Val Val Pro Thr Glu Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu	
320 325 330 335	
aac cct gtg cca atc ccc gcc cct gtt cgg aaa tgg gaa gac gtc gtc	1297
Asn Pro Val Pro Ile Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val	
340 345 350	
ggg gcc cag cca caa cgg ctt gac act gca gac cct ggc atg ctg tat	1345
Ala Ala Gln Pro Gln Arg Leu Asp Thr Ala Asp Pro Ala Met Leu Tyr	
355 360 365	
gct gtg gtg gat gcc gtg cct cgg aca cgg tgg aag gag ttc atg cgg	1393
Ala Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu Phe Met Arg	
370 375 380	
ctc ctg ggg ctg agc gag cac gag atc gag cgg ttg gag ctg cag aac	1441
Leu Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn	
385 390 395	
ggg cgt tgc ctc cgc gag got cat tac agc atg ctg gaa gcc tgg cgg	1489
Gly Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg	
400 405 410 415	
cgc cgc aca ccc cca cac gag gcc aag ctg gac gta gtg gcc cga gtg	1537
Arg Arg Thr Pro Arg His Glu Ala Thr Leu Asp Val Val Gly Arg Val	
420 425 430	
ctt tgc gac atg aac ctg cgt ggc tgc ctg gag aac atc cgc gag act	1585
Leu Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr	
435 440 445	
cta gaa age cct gcc cac tgc tcc acg aac ccc ctc cgc cga taa	1630
Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg	
450 455 460	
ggccacaccc ccacctcagg aacgggaacc gaaggaccat cctgctagat gccctgcttc	1690

cctgtgaacc tctcttttgg tctctttagg ggcagqctcg atctggcagg ctctgatctgg 1750
 caqccacttc ctttggtgcta ccgaacttgg gtatataget ttcccagct gccagaggaca 1810
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 ttc 2173

<210> 15
 <211> 461
 <212> PRT
 <213> Artificial Sequence

<210>
 <213> Description of Artificial Sequence: raTNF-R3

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 20 25 30
 Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly Lys
 35 40 45
 Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50 55 60
 Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val
 65 70 75 80
 Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val
 85 90 95
 Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val
 100 105 110
 Gln Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys Lys
 115 120 125
 Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys Val
 130 135 140
 Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu

145		150		155		160
Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly						
	165			170		175
Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met						
	180		185			190
Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser						
	195		200			205
Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu						
	210		215			220
Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg						
	225		230		235	240
Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu						
	245		250			255
Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile						
	260		265			270
Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu Gly Phe Ser						
	275		280			285
Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr Pro Ile Ser Pro						
	290		295			300
Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu						
	305		310		315	320
Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn						
	325		330			335
Pro Val Pro Ile Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala						
	340		345			350
Ala Gln Pro Gln Arg Leu Asp Thr Ala Asp Pro Ala Met Leu Tyr Ala						
	355		360			365
Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu Phe Met Arg Leu						
	370		375			380
Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly						
	385		390		395	400
Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg						
	405		410			415
Arg Thr Pro Arg His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu						
	420		425			430
Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu						
	435		440			445
Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg						

450

455

460

<210> 16
 <211> 1141
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (113)..(1180)

<220>
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 ITNF-R2

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 ctggacacac cgagtcacgg gaagccccag caactgacgt gccacactgc cctgagccca 180
 katgggggag tgagaggcca tagctgtctg gc atg ggc ctc tca acc gtg cct 232
 Met Gly Leu Ser Thr Val Pro
 1 5
 gac ctg ctg ctg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281
 Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr
 10 15 20
 ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329
 Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys
 25 30 35
 aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377
 Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
 40 45 50 55
 tgg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425
 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
 60 65 70
 tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473
 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
 75 80 85
 tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521
 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
 90 95 100
 aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569
 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
 105 110 115
 gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat 617
 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr

120	125	130	135	
tgc agt gaa aac att ttc cag tgc ttc aat tgc agc ctc tgc ctc aat				605
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	140	145	150	
gag aac gtc cac ctc tcc tgc cag gag aac cac aac aac gtc tgc aac				715
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr	155	160	165	
tgc aat gca agt ttc ttt cta aga gaa aac gag tgc gtc tcc tgc agt				761
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser	170	175	180	
aac tat aag aaa agc ctc gag tgc acg aag ttg tgc cta ccc cag att				805
Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile	185	190	195	
gag aat att aag agc act gag gaa tca ggt aac aac gtc ctc ttg ccc				851
Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro	200	205	210	215
ctg gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt				905
Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly	220	225	230	
tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt				955
Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val	235	240	245	
tgt ggg aaa tgc aca cct gaa aaa gag ggg gag ctt gaa gga act act				1001
Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr	250	255	260	
act aag ccc ctg gcc cca aac cca agc ttc agt ccc act cca gcc ttc				1049
Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe	265	270	275	
acc ccc acc ctg gcc ttc agt ccc ggc ccc agt tcc acc ttc acc tcc				1097
Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser	280	285	290	295
agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc				1145
Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg	300	305	310	
aga gag gtg gca cca ccc tat cag ggg gct gac ccc atc ctt gcg aca				1193
Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr	315	320	325	
gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac				1241
Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp	330	335	340	
agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acc ctg				1289
Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu	345	350	355	

tac gcc gtg gtg gag aac gtg ccc ccc ttg cgc tgg aac gaa ttc gtg 1357
Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val
350 365 370 375

cgg cgc cta ggg ctg agc gac caa gag atc gat cgg ctg gag ctg caa 1385
Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu Glu
380 385 390

aac ggg cgc tgc ctg cgc gag gag caa tac agc atg ctg gag aac tgg 1413
Asn Gly Arg Cys Leu Arg Glu Ala Glu Tyr Ser Met Leu Ala Thr Trp
395 400 405

cgg cgg cgc aac ccc cgg cgc gag gcc aac ctg gag ctg ctg gaa cgc 1441
Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg
410 415 420

gtg ctg cgc gac atg gag ctg ctg ggg tgc ctg gag gac atc gag gag 1469
Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu
425 430 435

ggc att tgc ggc ccc gcc gcc ctg ccc ccc ggc ccc agt att ctg aga 1577
Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg
440 445 450 455

tga ggctggcggc ctgggggag ctctaaggac cgtctggca gatcgcttc 1630

caacccccact tttttotgga aaggaggggt cctgcagggg caagcaggag ctacgagccg 1690

cctacttggg gctaaccct ccatgtacat agcttttctc agctgcctgc ggcgcgcga 1750

cagtcagcgc tctgcgcgcg gagagaggtg cgcctgtggc tcaagagcct gagtgggttg 1810

ttgcgagga tgagggaagc tatgcctcat gcccgcttg ggtgtctca ccagcaaggc 1870

tgtcggggg cccctggttc gtccctgagc ctttttcaca gtgcataagc agttttttt 1930

gtttttgttt tgtttgttt tgtttttaa tcaatcatgt tacactaata gaaacttggc 1990

actcctgtgc cctctgctg gacaagcaca tagcaagctg aactgtcta aggcaggggc 2050

gagcaaggaa caatgggggc ttcagctgga gctgtggact ttgtacata cactaaaatt 2110

ctgaagttaa aaaaaaaaaa aaaaggaatt c 2141

<210> 17

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human TNF-R in
1TNF-R2

<400> 17

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
1 5 10 15
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
20 25 30
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35 40 45
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65 70 75 80
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
85 90 95
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
100 105 110
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
115 120 125
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
130 135 140
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145 150 155 160
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
165 170 175
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
180 185 190
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
195 200 205
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
210 215 220
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
225 230 235 240
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
245 250 255
Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
260 265 270
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
275 280 285
Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Phe Asn
325 330 335 340 345 350

Ile Leu Glu Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
340 345 350 355 360

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
355 360 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
370 375 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
385 390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
420 425 430

Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
435 440 445

Pro Ala Pro Ser Leu Leu Arg
450 455

<110> 18

<111> 13

<112> PRT

<113> Artificial Sequence

<120>

<121> Description of Artificial Sequence: N-terminal
amino acid sequence of protein purified from urine
(main sequence)

<122>

<121> UNSURE

<122> (4)

<123> Identity of "Xaa" could not be determined.

<400> 13

Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln
1 5 10

<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: N-terminal
amino acid sequence of protein purified from urine
(subsidiary sequence)

<224>

<225> UNSURE

<226> (7)

<227> Identity of "Xaa" could not be determined.

<400> 18

Leu Val Pro His Leu Gly Xaa Arg Glu

<210> 16

<211> 151

<212> DNA

<213> Homo sapiens

<400> 16

caacggaaaa tattaccct caaataatc gatttgcgt accaagtgc acaaaggaaa 60

ctactctac aatgaetct cagggcggg gcaggatag tactgcggg agtgtgagag 120

gactcttc acagctcag aaaacaacaa g 151

<410> 31

<411> 3

<412> PRT

<413> Artificial Sequence

<414>

<415> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 31

Asp Ser Val Cys Pro Gln Gly Lys

1

5

<410> 32

<411> 7

<412> PRT

<413> Artificial Sequence

<414>

<415> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<416>

<417> UNSURE

<418> (1)...(2)

<419> Identity of "Xaa" could not be determined.

<400> 22

Xaa Xaa Leu Ser Cys Ser Lys

<210> 23
<211> 3
<212> PPT
<213> Artificial Sequence

<220>
<221> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 23
A p Thr Val Cys Gly Cys Arg
1 5

<100> 24
<110> 11
<112> PPT
<113> Artificial Sequence

<220>
<221> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 24
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
1 5 10

<100> 25
<110> 12
<112> PPT
<113> Artificial Sequence

<220>
<221> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 25
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys
1 5 10

<100> 26
<110> 13
<112> PPT
<113> Artificial Sequence

<220>
<221> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>
<221> UNSURE
<222> (6)

<223> Identity of "Xaa" could not be determined.

<220>

<221> UNSURE

<222> 11 A.V. (13)

<223> Identity of "Xaa" could not be determined.

<400> 26

Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys

1

5

10

<210> 27

<211> 14

<212> PFT

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 27

Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys

1

5

10

<210> 28

<211> 8

<212> PFT

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 28

Leu Val Pro His Leu Gly Asp Arg

1

5

<210> 29

<211> 15

<212> PFT

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 29

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg

1

5

10

15

<210> 30

<211> 17

<212> PFT

<212> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 30

His Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln
1 10

<210> 31

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<225>

<226> UNSURE

<227> (9)..(11)

<228> Identity of "Xaa" could not be determined.

<400> 31

Gln Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp
1 5 10

<210> 32

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 32

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp
1 5 10 15

Thr Val Cys Gly
20

<210> 33

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>

<221> UNSURE

<222> (6)

<223> Identity of "Xaa" could not be determined.

<224> 1

<225> UNSURE

<226> (18)

<227> Identity of "Xaa" could not be determined.

<228> 1

Tyr Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His Lys

1

5

10

15

Lys Xaa Tyr

<229> 34

<230> 18

<231> PFT

<232> Artificial Sequence

<233>

<234> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<235>

<236> UNSURE

<237> (16)..(17)

<238> Identity of "Xaa" could not be determined.

<239> 34

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Xaa

1

5

10

15

Xaa Arg

<240> 35

<241> 8

<242> PFT

<243> Artificial Sequence

<244>

<245> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<246> 35

Leu Cys Leu Pro Gln Ile Glu Asn

1

5

<247> 36

<248> 14

<249> PFT

<250> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>

<221> UNSURE

<227> (7)

<235> Identity of "Xaa" could not be determined.

<400> 36

Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg
1 5 10

<210> 37

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 35

Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn
1 5 10

<210> 38

<211> 15

<212> PRT

<213> Homo sapiens

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 38

Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln
1 5 10

<210> 39

<211> 7

<212> PRT

<213> Homo sapiens

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 39

Gln Gly Lys Tyr Ile His Pro
1 5

<210> 40
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 40
caaggtaaat atattcatcc

19

<210> 41
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 41
caggttaaatt acatccatcc

20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 42
caaggttaaatt atatacatcc

20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 43
caaggtcaaatt atattcatcc

20

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: Hybridization
probe

<10> 44

caacccaaagt acatccaccc

20

<10> 45

<11> 20

<12> DNA

<13> Artificial Sequence

<220>

<221> Description of Artificial Sequence: Hybridization
probe

<10> 45

caacccaaagt atatacatcc

20

<10> 46

<11> 20

<12> DNA

<13> Artificial Sequence

<220>

<221> Description of Artificial Sequence: Hybridization
probe

<10> 46

caacccaaagt atattcatcc

20

<10> 47

<11> 20

<12> DNA

<13> Artificial Sequence

<220>

<221> Description of Artificial Sequence: Hybridization
probe

<10> 47

caacccaaagt acatccaccc

20

<10> 48

<11> 20

<12> DNA

<13> Artificial Sequence

<220>

<221> Description of Artificial Sequence: Hybridization
probe

<10> 48

caagggaagt atatacatcc

20

<210> 49 \

<211> 20

<212> DNA

<213> Artificial Sequence

<214>

<215> Description of Artificial Sequence: Hybridization
probe

<210> 49

caagggaagt atatacatcc

20

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<214>

<215> Description of Artificial Sequence: Hybridization
probe

<210> 50

caagggaagt acatccaccc

20

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<214>

<215> Description of Artificial Sequence: Hybridization
probe

<210> 51

caagggaagt atatacatcc

20

<210> 52

<211> 14

<212> PRT

<213> Artificial Sequence

<214>

<215> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<210> 52

Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys

1

5

10

<210> 53

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 14
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys
1 10

<210> 14
<211> r
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 14
Phe Thr Ala Ser Glu Asn Asn Lys
1 5

<210> 55
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 55
Phe Thr Ala Ser Cys Asn Asn Lys
1 5

<210> 56
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 56
taa'gaaggga gaattattggt gttcctaggg

30

<210> ""
<211> 31
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization probe

<400> 47

aaatgacata gactttttgtt gttcctaggt

30

<210> 48

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization probe

<400> 48

aaatctcagga gactctttgtt gttcctaggg

30

<210> 49

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization probe

<400> 50

aaatgacggt cactctttgtt gttcctaggg

30

<210> 60

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization probe

<400> 60

aaatgacgctt ctctttttgtt gttcctaggg

30

<210> 61

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization probe

<400> 61
aaatcteggt cactctgtt gtctctaggg 30

<21> 62
<211> 30
<212> DNA
<213> Artificial Sequence

<22>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 62
aaatcagga gaacattgtt gtctctaggg 30

<21> 63
<211> 30
<212> DNA
<213> Artificial Sequence

<22>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 63
aaatagagta gtactttgtt gtctctaggg 30

<21> 64
<211> 30
<212> DNA
<213> Artificial Sequence

<22>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 64
aaatctegga gaacattgtt gtctctaggg 30

<21> 65
<211> 30
<212> DNA
<213> Artificial Sequence

<22>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 65
aaatgacgt caacattgtt gtctctaggg 30

<210> 66
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization
 probe

<400> 66
 agtggggt ctacttggg gtctctagg 33

<210> 67
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization
 probe

<400> 67
 aaatctgggt caacattggt gtctctagg 30

<210> 68
 <211> 158
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(153)

<400> 68
 gag ggg aaa tat att cac cct caa aat aat tgg att tgc tgt acc aag 48
 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys
 1 5 10 15

tgc cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag 96
 Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln
 20 25 30

gat acg gac tgc agg gag tgt gag agc ggc tcc ttc aca gcc tca gaa 144
 Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu
 35 40 45

aac aac aag gatcc 158
 Asn Asn Lys
 50

<210> 69
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 69
 Thr Gly Lys Tyr Ile His Pro His Asn Asn Ser Ile Cys Cys Thr Lys
 1 5 10 15
 Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln
 20 25 30
 Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu
 35 40 45
 Asn Asn Lys
 50

<210> 70
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <225> Description of Artificial Sequence: PCR primer
 EBI-1786

<400> 70
 ggaattcaga ctgaatggcg aatggg 26

<210> 71
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <225> Description of Artificial Sequence: PCR primer
 EBI-1729

<400> 71
 cctcgacgct tgctggcggt ttccc 25

<210> 72
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <225> Description of Artificial Sequence: PCR primer
 EBI-1733

<400> 72
 gtcgacatt gattattgac tag 23

<210> 73
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer:
EBI-1734

<400> 73

ggatttctat gaggatctatg cgt

10

<210> 74

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutagenesis
primer EBI-1751

<400> 74

gacttggaaac tegtctctg

19

<210> 75

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutagenesis
primer EBI-1857

<400> 75

ggcaggggca gcagcggg

18

<210> 76

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1823

<400> 76

aactttctgca ggtcgacatc gatggatcgg tacctcgagc ggccgcgaat tct

53

<210> 77

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1829

4008 77

ctagagaatt cggggcgct cgaggtacg gatccatga tctgacg caga 54

<210> 78

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1820

4009 78

agctctagag attcgggggc gctcgaggta cgggacat cgatgcgac ctgcagaagc 60

tta

63

<210> 79

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1821

<400> 79

ctagcaagct tctcgaggtc gacatcgatg gatccggta ctcgagggc cggcattct 60

ctag

64

<210> 80

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-1936

<400> 80

cagatccga gctcaaac ccaac

25

<210> 81

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-1929

<400> 81
aggaattct tat caattct caatctgggg taggcacaa ttc 43

<210> 81
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of Artificial Sequence: PCR primer
EBI-2452

<400> 82
acaatcgac ttacatttgc ttctgacaa actgtgttc ctacaaact caaagagaa 60
aatagggct ctccacggtg c 81

<210> 83
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of Artificial Sequence: PCR primer
EBI-1922

<400> 83
gagcctgcaa ttgaagc 17

<210> 84
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of Artificial Sequence: PCR primer
EBI-2316

<400> 84
attctgggg cgcctag 17

<210> 85
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of Artificial Sequence: PCR primer
EBI-2467

<400> 85
gtcgtagca ccaagga 17

<210> 86
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1986

<400> 86
gttttccag taacgac

17

<210> 87
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Sequencing
primer EBI-2112

<400> 87
gtccaattat gtcacacc

18